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Haplotype Variations and Evolutionary Analysis of Granule-Bound Starch Synthase 1 (GBSSI) Gene in Improved KRICE_CORE

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[Introduction]

Granule-bound starch synthase I (GBSSI) is responsible to encode the Waxy gene in amylose synthesis of starch biosynthesis. In spite of many findings on waxy alleles, the genetic diversity and evolutionary studies are still different by their functional responses.

[Materials and Methods]

To investigate the genetic variations and relatedness of *GBSSI* gene in 475 improved KRICE_CORE (Korean World Rice Collection), haplotype variations and evolutionary analyses were performed after variant calling on 475 genomic sequences for *GBSSI*.

[Results and Discussion]

We found 12 functional SNPs (F-SNP) (non-synonymous substitutions) of *GBSSI* including 9 novel F-SNPs. Five novel F-SNPs were localized in wild rice, four G/A (exon 2, 9 and 12) and one T/C FNPs (exon 13) in wild rice. The diversity of *GBSSI* in wild rice showed higher (p = 0.0056) than any of cultivated groups and the relatedness of wild with others (except bred) will be far by lower Tajima's D values (-0.0403). The specification of localized F-SNPs and in cultivated rice and reduction of diversity suggested that *GBSSI* of cultivated rice could have been domesticated during rice cultivation after speciation between cultivated and wild rice. We divided cultivated rice into landrace, weedy and bred variety, and conducted all-against-all comparison for fixation index (F_{ST}) with wild. Free interbreeding was implied only between landrace and weedy by a very lowest value of F_{ST} (-0.008), compared to any others which signified great differentiation between them. Referring and combining these findings can promote future breeding programs through considering of that information about new functional alleles together with their genetic responses among the groups.

Keywords: Granule-bound starch synthase 1 (GBSSI), SNP, Domestication, cultivated rice, wild rice

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